0590
12/2

#2   QIPE

RAW SEQUENCE LISTING   DATE: 12/07/2001
PATENT APPLICATION: US/09/997,900   TIME: 12:49:59

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Output Set: N:\CRF3\12072001\I997900.raw

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 3 <110> APPLICANT: Kakefuda, Genichi
 4        Costello, Colleen
 5        Sun, Ming
 6        Hu, Weiming
 8 <120> TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
 9        in Plants
11 <130> FILE REFERENCE: 043753/241148 (5849-20A)
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C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/997,900
C--> 14 <141> CURRENT FILING DATE: 2001-11-30
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16 <150> PRIOR APPLICATION NUMBER: 60/106,239
17 <151> PRIOR FILING DATE: 1998-10-29
19 <150> PRIOR APPLICATION NUMBER: 09/426,568
20 <151> PRIOR FILING DATE: 1999-10-22
22 <160> NUMBER OF SEQ ID NOS: 11
24 <170> SOFTWARE: PatentIn Ver. 2.1
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27 <211> LENGTH: 1673
28 <212> TYPE: DNA
29 <213> ORGANISM: Arabidopsis sp.
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32 <221> NAME/KEY: CDS
33 <222> LOCATION: (42)..(1514)
34 <223> OTHER INFORMATION: Mature Peptide
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38                                                 Met Ala Ala Ile Ser
39                                                  1               5
41 gta agt tct tca cca tct att cgc tgc ttg aga tcg gca tgt tcc gat    104
42 Val Ser Ser Ser Pro Ser Ile Arg Cys Leu Arg Ser Ala Cys Ser Asp
43                 10                  15                  20
45 tct tct cct gct ctt gta tcc tcg acg cgt gta tcg ttc ccg gcg aag    152
46 Ser Ser Pro Ala Leu Val Ser Ser Thr Arg Val Ser Phe Pro Ala Lys
47                 25                  30                  35
49 att tca tat ctc tcc ggt ata tct tcg cac cgt ggc gat gaa atg ggt    200
50 Ile Ser Tyr Leu Ser Gly Ile Ser Ser His Arg Gly Asp Glu Met Gly
51              40                  45                  50
53 aag aga atg gaa gga ttc gtt aga agc gtc gat ggg aag atc tct gat    248
54 Lys Arg Met Glu Gly Phe Val Arg Ser Val Asp Gly Lys Ile Ser Asp
55       55                  60                  65
57 gcg tct ttc tcc gaa gct tca tct gcg act cca aaa tcg aag gtg agg    296
58 Ala Ser Phe Ser Glu Ala Ser Ser Ala Thr Pro Lys Ser Lys Val Arg
59   70                  75                  80                  85
61 aag cac aca att tca gta ttt gtt gga gac gaa agc gga atg att aat    344
62 Lys His Thr Ile Ser Val Phe Val Gly Asp Glu Ser Gly Met Ile Asn
63                 90                  95                  100
65 agg att gca gga gtg ttt gca agg aga gga tac aat att gag agt ctt    392
66 Arg Ile Ala Gly Val Phe Ala Arg Arg Gly Tyr Asn Ile Glu Ser Leu
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67                   105                      110                      115
69 gct gtt ggt ctg aac aga gac aag gct cta ttc acc ata gtt gtc tgt      440
70 Ala Val Gly Leu Asn Arg Asp Lys Ala Leu Phe Thr Ile Val Val Cys
71           120                      125                      130
73 gga act gaa agg gta ctt cag cag gtc atc gag caa ctc cag aag ctc      488
74 Gly Thr Glu Arg Val Leu Gln Gln Val Ile Glu Gln Leu Gln Lys Leu
75           135                      140                      145
77 gtt aat gtt cta aag gtt gaa gat atc tca agt gag ccg caa gtg gag      536
78 Val Asn Val Leu Lys Val Glu Asp Ile Ser Ser Glu Pro Gln Val Glu
79 150                      155                      160                      165
81 cgt gag ctg atg ctt gta aaa gtg aat gca cat cca gaa tcc agg gca      584
82 Arg Glu Leu Met Leu Val Lys Val Asn Ala His Pro Glu Ser Arg Ala
83                   170                      175                      180
85 gag atc atg tgg cta gtt gac aca ttc aga gca aga gtt gta gat ata      632
86 Glu Ile Met Trp Leu Val Asp Thr Phe Arg Ala Arg Val Val Asp Ile
87                   185                      190                      195
89 gcg gaa cat gca ttg act atc gag gta act gga gat cct gga aaa atg      680
90 Ala Glu His Ala Leu Thr Ile Glu Val Thr Gly Asp Pro Gly Lys Met
91           200                      205                      210
93 att gct gta gaa aga aat ttg aaa aag ttt cag atc aga gag att gta      728
94 Ile Ala Val Glu Arg Asn Leu Lys Lys Phe Gln Ile Arg Glu Ile Val
95           215                      220                      225
97 agg aca gga aag ata gca ctg aga agg gaa aag atg ggt gca act gct      776
98 Arg Thr Gly Lys Ile Ala Leu Arg Arg Glu Lys Met Gly Ala Thr Ala
99 230                      235                      240                      245
101 cca ttt tgg cga ttt tca gca gca tcc tat cca gat ctc aag gag caa      824
102 Pro Phe Trp Arg Phe Ser Ala Ala Ser Tyr Pro Asp Leu Lys Glu Gln
103                   250                      255                      260
105 gcg cct gtt agt gtt ctt cga agt agc aaa aaa gga gcc att gtc cct      872
106 Ala Pro Val Ser Val Leu Arg Ser Ser Lys Lys Gly Ala Ile Val Pro
107                   265                      270                      275
109 caa aag gaa aca tca gca ggg gga gat gtt tat ccc gtt gag cca ttt      920
110 Gln Lys Glu Thr Ser Ala Gly Gly Asp Val Tyr Pro Val Glu Pro Phe
111           280                      285                      290
113 ttt gac ccc aag gta cat cgt att ctc gac gct cac tgg gga ctt ctc      968
114 Phe Asp Pro Lys Val His Arg Ile Leu Asp Ala His Trp Gly Leu Leu
115           295                      300                      305
117 act gac gaa gat acg agt gga cta cgg tcg cat act cta tca ttg ctt      1016
118 Thr Asp Glu Asp Thr Ser Gly Leu Arg Ser His Thr Leu Ser Leu Leu
119 310                      315                      320                      325
121 gta aat gat att cca gga gtt ctt aat att gtg act ggt gtt ttc gct      1064
122 Val Asn Asp Ile Pro Gly Val Leu Asn Ile Val Thr Gly Val Phe Ala
123                   330                      335                      340
125 cga agg gga tac aat atc cag agc ttg gcc gta gga cat gct gaa acc      1112
126 Arg Arg Gly Tyr Asn Ile Gln Ser Leu Ala Val Gly His Ala Glu Thr
127           345                      350                      355
129 aag ggc att tca cgc att aca aca gtt ata cct gca aca gat gaa tcg      1160
130 Lys Gly Ile Ser Arg Ile Thr Thr Val Ile Pro Ala Thr Asp Glu Ser
131           360                      365                      370
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133 gtc agc aaa ttg gtg cag caa ctt tac aaa ctc gta gat gtg cat gag   1208
134 Val Ser Lys Leu Val Gln Gln Leu Tyr Lys Leu Val Asp Val His Glu
135     375             380             385
137 gtc cat gat ctt act cat ttg cca ttt tct gaa aga gaa ctg atg ctg   1256
138 Val His Asp Leu Thr His Leu Pro Phe Ser Glu Arg Glu Leu Met Leu
139 390             395             400             405
141 att aag att gcc gtg aac gct gct gct aga aga gat gtc ctg gac att   1304
142 Ile Lys Ile Ala Val Asn Ala Ala Ala Arg Arg Asp Val Leu Asp Ile
143             410             415             420
145 gct agt att ttc agg gct aaa gct gtt gac gta tct gat cac aca att   1352
146 Ala Ser Ile Phe Arg Ala Lys Ala Val Asp Val Ser Asp His Thr Ile
147             425             430             435
149 act ttg cag ctt act ggg gat cta gac aag atg gtt gca ctg caa agg   1400
150 Thr Leu Gln Leu Thr Gly Asp Leu Asp Lys Met Val Ala Leu Gln Arg
151         440             445             450
153 tta ttg gag ccc tat ggt ata tgt gag gtt gca aga acc ggt cgt gtg   1448
154 Leu Leu Glu Pro Tyr Gly Ile Cys Glu Val Ala Arg Thr Gly Arg Val
155     455             460             465
157 gca ttg gct cgt gaa tcg gga gtg gac tcc aag tac ctt cgt gga tac   1496
158 Ala Leu Ala Arg Glu Ser Gly Val Asp Ser Lys Tyr Leu Arg Gly Tyr
159 470             475             480             485
161 tcc ttt ctt tta aca ggc taaaccgttg cagagtgcat ccatcgaaca   1544
162 Ser Phe Leu Leu Thr Gly
163             490
165 tcagaaactt tggaaggtaa aagtttcatt acacagtcta tgaacctcaa agacagacag 1604
167 agagactgcg tcgatatatg tttgtgactt tgtttatgaa acaattagct gattttgggc 1664
169 ttcatttcg   1673
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173 <211> LENGTH: 491
174 <212> TYPE: PRT
175 <213> ORGANISM: Arabidopsis sp.
177 <400> SEQUENCE: 2
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179 1               5               10              15
181 Ser Ala Cys Ser Asp Ser Ser Pro Ala Leu Val Ser Ser Thr Arg Val
182             20              25              30
184 Ser Phe Pro Ala Lys Ile Ser Tyr Leu Ser Gly Ile Ser Ser His Arg
185             35              40              45
187 Gly Asp Glu Met Gly Lys Arg Met Glu Gly Phe Val Arg Ser Val Asp
188     50              55              60
190 Gly Lys Ile Ser Asp Ala Ser Phe Ser Glu Ala Ser Ser Ala Thr Pro
191 65              70              75              80
193 Lys Ser Lys Val Arg Lys His Thr Ile Ser Val Phe Val Gly Asp Glu
194             85              90              95
196 Ser Gly Met Ile Asn Arg Ile Ala Gly Val Phe Ala Arg Arg Gly Tyr
197             100             105             110
199 Asn Ile Glu Ser Leu Ala Val Gly Leu Asn Arg Asp Lys Ala Leu Phe
200             115             120             125
202 Thr Ile Val Val Cys Gly Thr Glu Arg Val Leu Gln Gln Val Ile Glu
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205 Gln Leu Gln Lys Leu Val Asn Val Leu Lys Val Glu Asp Ile Ser Ser
206 145                    150                    155                    160
208 Glu Pro Gln Val Glu Arg Glu Leu Met Leu Val Lys Val Asn Ala His
209                    165                    170                    175
211 Pro Glu Ser Arg Ala Glu Ile Met Trp Leu Val Asp Thr Phe Arg Ala
212                    180                    185                    190
214 Arg Val Val Asp Ile Ala Glu His Ala Leu Thr Ile Glu Val Thr Gly
215             195                    200                    205
217 Asp Pro Gly Lys Met Ile Ala Val Glu Arg Asn Leu Lys Lys Phe Gln
218         210                    215                    220
220 Ile Arg Glu Ile Val Arg Thr Gly Lys Ile Ala Leu Arg Arg Glu Lys
221 225                    230                    235                    240
223 Met Gly Ala Thr Ala Pro Phe Trp Arg Phe Ser Ala Ala Ser Tyr Pro
224                    245                    250                    255
226 Asp Leu Lys Glu Gln Ala Pro Val Ser Val Leu Arg Ser Ser Lys Lys
227                    260                    265                    270
229 Gly Ala Ile Val Pro Gln Lys Glu Thr Ser Ala Gly Gly Asp Val Tyr
230                    275                    280                    285
232 Pro Val Glu Pro Phe Phe Asp Pro Lys Val His Arg Ile Leu Asp Ala
233         290                    295                    300
235 His Trp Gly Leu Leu Thr Asp Glu Asp Thr Ser Gly Leu Arg Ser His
236 305                    310                    315                    320
238 Thr Leu Ser Leu Leu Val Asn Asp Ile Pro Gly Val Leu Asn Ile Val
239                    325                    330                    335
241 Thr Gly Val Phe Ala Arg Arg Gly Tyr Asn Ile Gln Ser Leu Ala Val
242                    340                    345                    350
244 Gly His Ala Glu Thr Lys Gly Ile Ser Arg Ile Thr Thr Val Ile Pro
245         355                    360                    365
247 Ala Thr Asp Glu Ser Val Ser Lys Leu Val Gln Gln Leu Tyr Lys Leu
248         370                    375                    380
250 Val Asp Val His Glu Val His Asp Leu Thr His Leu Pro Phe Ser Glu
251 385                    390                    395                    400
253 Arg Glu Leu Met Leu Ile Lys Ile Ala Val Asn Ala Ala Ala Arg Arg
254                    405                    410                    415
256 Asp Val Leu Asp Ile Ala Ser Ile Phe Arg Ala Lys Ala Val Asp Val
257             420                    425                    430
259 Ser Asp His Thr Ile Thr Leu Gln Leu Thr Gly Asp Leu Asp Lys Met
260         435                    440                    445
262 Val Ala Leu Gln Arg Leu Leu Glu Pro Tyr Gly Ile Cys Glu Val Ala
263         450                    455                    460
265 Arg Thr Gly Arg Val Ala Leu Ala Arg Glu Ser Gly Val Asp Ser Lys
266 465                    470                    475                    480
268 Tyr Leu Arg Gly Tyr Ser Phe Leu Leu Thr Gly
269                    485                    490
273 <210> SEQ ID NO: 3
274 <211> LENGTH: 4895
275 <212> TYPE: DNA
276 <213> ORGANISM: Arabidopsis sp.
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RAW SEQUENCE LISTING   DATE: 12/07/2001
PATENT APPLICATION: US/09/997,900   TIME: 12:49:59

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280 <222> LOCATION: (1)..(757)
281 <223> OTHER INFORMATION: Promoter Region
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284 <221> NAME/KEY: misc_feature
285 <222> LOCATION: (717)
286 <223> OTHER INFORMATION: Transcriptional Starting Point
288 <220> FEATURE:
289 <221> NAME/KEY: misc_signal
290 <222> LOCATION: (758)..(760)
291 <223> OTHER INFORMATION: Start Codon
293 <220> FEATURE:
294 <221> NAME/KEY: misc_signal
295 <222> LOCATION: (4737)..(4739)
296 <223> OTHER INFORMATION: Stop Codon
298 <220> FEATURE:
299 <223> OTHER INFORMATION: n at position 694 can be a, c, g, or t
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304 attcgccatg atttcgaaat ctctttctct tcttctctct ttcgtcttct tctgcgaaaa 180
305 aatcgaatgg ataatcacat tttctttttc tcgagaaaat tgatctggtg attatgtgag 240
306 atccgtctct agcgcgttgc ttatcgagaa ataattaatt ttaatttgac gggtgaagat 300
307 attattggcg acgtctgttt ccgattgact ttgatttgac ttttcctttc aatcattatt 360
308 tggcgagtcc cgcgtaaata tggactcttc ttgattgtcc cactttttc ggtggcttta 420
309 ccggatttaa aatcattttc ttttcctaaa ttatgaattt taccctaaac ttctcataat 480
310 tacaattagt tccgacgaac ccaagatact ttttagcaaa attaggaaaa tagttgactc 540
311 gaaaaggttg ttataacgtg gagctgacgt gttggtctta tctactcgaa gccttttggg 600
312 cttttcttaa agccattgat ttctaaggtc gtcaacaacc gaaccggacc ggacggtttg 660
W--> 313 accggtctaa ccaacatata tacgttcttt ttcnacttgc cgtttcgtcg tcgtcagtct 720
314 tcttcagtag caaaaaacct tcggcttcgt ctcgtcaatg gcggccattt ctgtaagttc 780
315 ttcaccatct attcgctgct tgagatcggc atgttccgat tcttctcctg ctcttgtatc 840
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317 tggcgatgaa atgggtaaga gaatggaagg attcgttaga agcgtcgatg ggaagatctc 960
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329 tctctaaatt tgattaagct tctgttttaa tgaattcaca gatcatgtgg ctagttgaca 1680
330 cattcagagc aagagttgta gatatagcgg aacatgcatt gactatcgag gtacatctac 1740
331 ttattatgat ttgtgttggt cttgatattt gtttcgcact gtagcctgtg ggtttcaaga 1800
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/997,900

DATE: 12/07/2001
TIME: 12:50:00

Input Set : **A:\2411481.app**
Output Set: **N:\CRF3\12072001\I997900.raw**

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3